

5'	9	18	27	36	45	54										
GGG	ACT	TCC	AGT	AGG	CGG	CAT	GTT	TGA	AAA	GTG	ATG	ACG	GTT	GAC	GTT	TGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	63	72	81	90	99	108										
TGA	TTT	TTG	ACT	TTG	GTA	GCT	GCT	CCC	CGA	ACT	CGC	CGT	CTT	CCT	GTC	GGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	117	126	135	144	153	162										
GGC	CGG	CAC	TGT	AGG	TGA	GCG	GAG	GAC	GGA	GGA	AGG	AAG	CCT	GCA	GAC	AGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	171	180	189	198	207	216										
CGC	CTT	CTC	CAT	CCC	AAG	GCG	GCG	GCA	GGT	GCC	GGG	ACG	CTG	GGC	CTG	GTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	225	234	243	252	261	270										
TTT	TCG	TCG	TGC	TCA	GCG	GTG	GGA	GGA	GGC	GGA	AGA	AAC	CAG	AGC	CTG	GGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	279	288	297	306	315	324										
TAA	CAG	GAA	ACT	TCC	AAG	ATG	GAA	ACT	TTG	TCT	TTT	CCC	AGA	TAT	AAT	GTA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	333	342	351	360	369	378										
GAG	ATT	GTG	ATT	CAT	ATT	CGC	AAT	AAG	ATC	TTA	ACA	GGA	GCT	GAT	GGT	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
E	I	V	I	H	I	R	N	K	I	L	T	G	A	D	G	K
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIGURE 1A

387	CTC	ACC	AAG	AAT	GAT	CYT	TAT	CCA	AAT	CCA	AAG	CCT	GAA	GTC	TTG	CAC	ATG	ATC	432
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	L	T	K	N	D	L	Y	P	N	P	K	P	E	V	L	H	M	I	
441	TAC	ATG	AGA	GCC	TTA	CAA	ATA	GTA	TAT	GGA	ATT	CGA	CTG	GAA	CAT	TTT	TAC	ATG	486
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Y	M	R	A	L	Q	I	V	Y	G	I	R	L	E	H	F	Y	M	
495	ATG	CCA	GTG	AAC	TCT	GAA	GTC	ATG	TAT	CCA	CAT	TTA	ATG	GAA	GGC	TTC	TTA	CCA	540
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	M	P	V	N	S	E	V	M	Y	P	H	L	M	E	G	F	L	P	
549	TTC	AGC	AAT	TTA	GTT	ACT	CAT	CTG	GAC	TCA	TTT	TTG	CCT	ATC	TGC	CGG	GTG	AAT	594
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	F	S	N	L	V	T	H	L	D	S	F	L	P	I	C	R	V	N	
603	GAC	TTT	GAG	ACT	GCT	GAT	ATT	CTA	TGT	CCA	AAA	GCA	AAA	CGG	ACA	AGT	CGG	TTT	648
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	D	F	E	T	A	D	I	L	C	P	K	A	K	R	T	S	R	F	
657	TTA	AGT	GGC	ATT	ATC	AAC	TTT	ATT	CAC	TTT	ACA	GAA	GCA	TGC	CGT	GAA	ACG	TAT	702
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	L	S	G	I	I	N	F	I	H	F	R	E	A	C	R	E	T	Y	

FIGURE 1B

711	ATG GAA TTT	720	CTT TGG CAA	729	TAT AAA TCC	738	TCT GCG GAC	747	AAA ATG CAA	756	CAG TTA AAC
	M E F L W Q		L W Q		Y K S S A D		K S A D K M		Q Q Q L N		
765	GCC GCA CAC	774	CAG GAG GCA	783	TTA ATG AAA	792	CTG GAG AGA	801	CTT GAT TCT	810	GTT CCA GTT
	A A H Q E A		L M K L E R		L M K L E R		L D S V P				
819	GAA GAG CAA	828	GAA GAG TTC	837	AAG CAG CTT	846	TCA GAT GGA	855	ATT CAG GAG	864	CTA CAA CAA
	E E Q E E F		K Q L S D G		I Q E L Q Q						
873	TCA CTA AAT	882	CAG GAT TTT	891	CAT CAA AAA	900	GTG CTA GAT	909	CAA GAG GGA	918	AAT TCC
	S L N Q D F		H Q K T I V		L Q E G N S						
927	CAA AAG AAG	936	TCA AAT ATT	945	TCA GAG AAA	954	CGT TTG AAT	963	GAA CTA AAA	972	TTG
	Q K K S N I		S E K T K R		L N E L K L						
981	TCG GTG GTT	990	TCT TTG AAA	999	ATA CAA GAG	1008	AGT TTG AAA	1017	ACA AAA ATT	1026	GTG GAT
	S V V S L K		E I Q E S L		K T K I V D						

FIGURE 1C

1035	1044	1053	1062	1071	1080
TCT CCA GAG AAG TTA AAG AAT TAT AAA GAA AAA ATG AAA GAT ACG GTC CAG AAG					
---	---	---	---	---	---
S P E E K L K N Y K E K M K D T V Q K					
---	---	---	---	---	---
1089	1098	1107	1116	1125	1134
CTT AAA AAT GCC AGA CAA GAA GTG GTG GAG AAA TAT GAA ATC TAT GGA GAC TCA					
---	---	---	---	---	---
L K N A R Q E V V E K Y E I Y G D S					
---	---	---	---	---	---
1143	1152	1161	1170	1179	1188
GTT GAC TGC CTG CCT TCA TGT CAG TTG GAA GTG CAG TTA TAT CAA AAG AAA ATA					
---	---	---	---	---	---
V D C L P S C Q L E V Q L Y Q K K I					
---	---	---	---	---	---
1197	1206	1215	1224	1233	1242
CAG GAC CTT TCA GAT AAT AGG GAA AAA TTA GCC AGT ATC TTA AAG GAG AGC CTG					
---	---	---	---	---	---
Q D L S D N R E K L A S I L K E S L					
---	---	---	---	---	---
1251	1260	1269	1278	1287	1296
AAC TTG GAG GAC CAA ATT GAG AGT GAT GAG TCA GAA CTG AAG AAA TTG AAG ACT					
---	---	---	---	---	---
N L E D Q I E S D E S E L K K L K T					
---	---	---	---	---	---
1305	1314	1323	1332	1341	1350
GAA GAA AAT TCG TTC AAA AGA CTG ATG ATT GTG AAG AAG GAA AAA CTT GCC ACA					
---	---	---	---	---	---
E E N S F K K R L M I V K K E K L A T					

FIGURE ID

1359	1368	1377	1386	1395	1404
GCA CAA TTC	AAA ATA AAT	AAG AAG CAT	GAA GAT GTT	AAG CAA TAC	AAA CGC ACA
A Q F	K I N	K K H	E D V	K Q Y	K R T
1413	1422	1431	1440	1449	1458
GTA ATT GAG	GAT TGC AAT	AAA GTT CAA	GAA AAA AGA	GGT GCT GTC	TAT GAA CGA
V I E	D C N	K V Q	E K R	G A V	Y E R
1467	1476	1485	1494	1503	1512
GTA ACC ACA	ATT AAT CAA	GAA ATC CAA	AAA ATT AAA	CTT GGA ATT	CAA CAA CTA
V T T	I N Q	E I Q	K I K	L G I	Q Q L
1521	1530	1539	1548	1557	1566
AAA GAT GCT	GCT GAA AGG	GAG AAA CTG	AAG TCC CAG	GAA ATA TTT	CTA AAC TTG
K D A	A E R	E K L	K S Q	E I F	L N L
1575	1584	1593	1602	1611	1620
AAA ACT GCT	TTG GAG AAA	TAC CAC GAC	GGT ATT GAA	AAG GCA GCA	GAG GAC TCC
K T A	L E K	Y H D	G I E	K A A	E D S
1629	1638	1647	1656	1665	1674
TAT GCT AAG	ATA GAT GAG	AAG ACA GCT	GAA CTG AAG	AGG AAG ATG	TTC AAA ATG
Y A K	I D E	K T A	E L K	R K M	F K M

FIGURE 1E

1683	TCA ACC TGA	TTA ACA AAA	TTT CAT GTC	TTT TTG TAA ATG	GCT TGC	CAT CTT	TTA
---	---	---	---	---	---	---	---
S	T	*					
---	---	---	---	---	---	---	---
1737	ATT TTC TAT	TTA GAA AGA AAA	GTT GAA GCG AAT	GGA AGT ATC AGA	AGT ACC	AAA	
---	---	---	---	---	---	---	---
1791	TAA TGT TGG	CTT CAT CAG	TTT TTA TAC	ACT CTC ATA	AGT TAA	TAA GAT	GAA
---	---	---	---	---	---	---	---
1845	TTT AAT GTA	GGC TTT TAT	TAA TTT ATA	ATT AAA ATA	ACT TGT GCA	GCT ATT	CAT
---	---	---	---	---	---	---	---
1899	GTC TCT ACT	CTG CCC CTT	GTT GTA AAT	AGT TTG AGT	AAA ACA AAA	CTA GTT	ACC
---	---	---	---	---	---	---	---
1953	TTT GAA ATA	TAT ATA TTT	TTT TCT GTT	ACA AAA AA	3'		
---	---	---	---	---	---	---	---

FIGURE 1F

1 METLSFPRYNVAEIV I H I R N K I L T G A D G K N GRIP  
1 METLSFPRYN T A E I V V H I R N K L L T G A D G K N HW051

31 L T K N D L Y P N P K P E V L H M I Y M R A L Q I V Y G I R GRIP  
31 L S K S D F L P N P K P E V L Y M I Y M R A L Q L V Y G V R HW051

61 L E H F Y M M P V N S E V M Y P H L M E G F L P F S N L V T GRIP  
61 L E H F Y M M P V N I E V M Y P H I M E G F L P V S N L F F HW051

91 H L D S F L P I C R V N D F E T A D I L C P K A K R T S R F GRIP  
91 H L D S F M P I C R V N D F E I A D I L Y P K A N R T S R F HW051

121 L S G I I N F I H F R E A C R E T Y M E F F L W Q Y K S S A D GRIP  
121 L S G I I N F I H F R E T C L E K Y E E F L L Q N K S S V D HW051

151 K M Q Q L N A A H Q E A L M K L E R L D S V P V E E Q E E F GRIP  
151 K I Q Q L S N A H Q E A L M K L E K L N S V P V E E Q E E F HW051

181 K Q L S D G I Q E L Q Q S L N Q D F H Q K T I V L Q E G N S GRIP  
181 K Q L K D I Q E L Q H L L N Q D F R Q K T T L L Q E R Y T HW051

211 Q K K S N I S E K T K R L N E L K L S V S L K E I Q E S L GRIP  
211 K M K S D F S E K T K H V N E L K L S V S L K E V Q D S L HW051

FIGURE 2A





Tissue Category	Clone Count	Found in	Ab Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	1/47	2	0.0014
Digestive System	501101	3/148	4	0.0008
Embryonic Structures	106713	2/21	2	0.0019
Endocrine System	225386	1/53	1	0.0004
Exocrine Glands	254635	2/64	2	0.0008
Genitalia, Female	427284	3/106	3	0.0007
Genitalia, Male	448207	2/114	6	0.0013
Germ Cells	38282	1/5	1	0.0026
Hemic and Immune System	680277	15/159	20	0.0029
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	0/47	0	0.0000
Nervous System	955753	2/19	2	0.0002
Pancreas	110207	1/24	1	0.0009
Respiratory System	390086	4/93	5	0.0013
Sense Organs	19256	1/8	1	0.0052
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	3/13	5	0.0041
Urinary Tract	279062	2/64	2	0.0007
Totals	5321883	47/1292	6	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Abund	Pct Abund
BMARTXR02	682	bone marrow tumor line, neuroblastoma, t/6-OHDA,	1	0.1466
TYLXUNT01	3669	T-lymphocytes, allogenic, 40-50M, untreated	3	0.0818
TBLXNOT01	3119	T-B lymphoblast line, leukemia, untreated	2	0.0641
U937NOT01	2067	monocyte line, histiocytic lymphoma, untreated	1	0.0484
BMARTXT03	2162	bone marrow tumor line, neuroblastoma, t/6-OHDA	1	0.0463
BMARTXT06	2787	bone marrow tumor line, neuroblastoma, untreated	1	0.0359
SPLNTUT02	3017	spleen tumor, Hodgkin's, 45M	1	0.0331
MCLDTXT04	3310	UCB, derived dendritic cells, t/PMA, Ionomycin	1	0.0302
THYMFET03	3577	thymus, fetal, M	1	0.0280
MYEPTXT01	3944	CML precursor line, K-562, 53F, t/5AZA 72 h	1	0.0254
SPLNFET02	7859	spleen, fetal, 23wM	1	0.0127
TYLXNNT08	9784	T-lymphocytes, allogenic anergic, t/OKT3 3 day	1	0.0102

Two pooled libraries, two normalized libraries, and one subtracted library are not shown.

FIGURE 3B

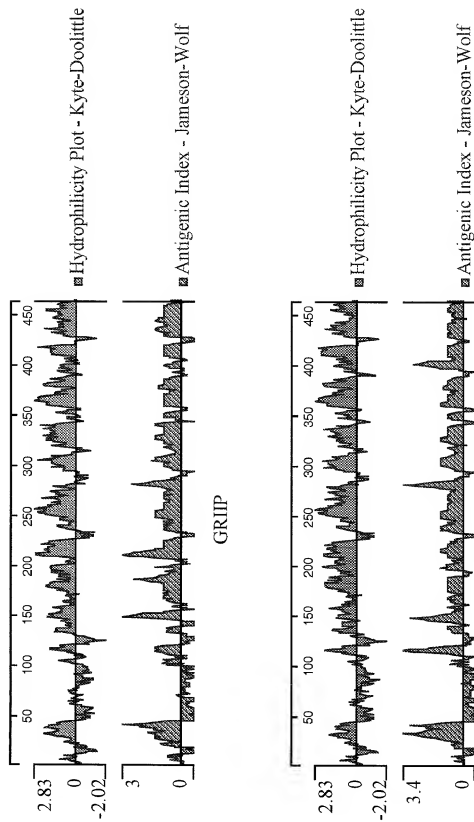


FIGURE 4